INFERENCE REFERENCE SHEET

Stat 120 | Fall 2025

Prof Amanda Luby

| Name | Type of Variable(s) | Statistic | Parameter |
|---------------------------|-----------------------------|-------------------------|-----------------|
| Mean | Quantitative | \bar{x} | μ |
| Proportion | Categorical | \hat{p} | p |
| Standard Deviation | Quantitative | s | σ |
| Difference in Proportions | 2 Categorical | $\hat{p}_1 - \hat{p}_2$ | $p_{1} - p_{2}$ |
| | (1 Response, 1 Explanatory) | - | - + - - |
| Difference in Means | 1 Quantitative (Response) | $\bar{x}_1 - \bar{x}_2$ | $\mu_1 - \mu_2$ |
| | 1 Categorical (Explanatory) | | <u>-</u> |
| Correlation | 2 Quantitative | r | ho |
| Slope | 2 Quantitative | b_1 | β_1 |

Hypothesis Test

Confidence Interval

- 1. I am ____ % confident
- 2. that the [population parameter in context]
- 3. is between ____ and ____ [units]

- 1. At $\alpha = [\text{significance level}]$
- 2. I [reject/do not reject] ${\cal H}_0$
- 3. with a p-value of [p-value]
- 4. and conclude [population parameter] is ...

 $\frac{H_0 \ \mathrm{True} \quad H_0 \ \mathrm{False}}{\mathrm{Reject} \ H_0}$ Do not reject H_0

R Commands

library(CarletonStats)

Confidence Interval

Mean/Proportion: boot(~<variable_name>, data = <dataset_name>, seed = <seed>)

Difference: boot(<response> ~ <explanatory>, data = <dataset_name>, seed = <seed>)

Paired Diff.: bootPaired(<response1> ~ <response2>, data = <dataset>, seed = <seed>)

Correlation: bootCor(<response> ~ <explanatory>, data = <dataset_name>, seed = <seed>)

Hypothesis Test

Difference: permTest(<response> ~ <explanatory>, data = <dataset_name>, seed = <seed>)

Paired Diff.: permTestPaired(<response1> ~ <response2>, data = <dataset>, seed = <seed>)

Correlation: permTestCor(<response> ~ <explanatory>, data = <dataset_name>, seed = <seed>)